

Wed Apr 16 08:08:22 2003

us-09-001-737-8.rsp

Page 1

GenCov version 5.1.4.ps-4578
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OM protein - protein search, using sw model

Run on: April 8, 2003, 14:23:17 ; Search time 14 Seconds
(without alignments)
1614.614 Million cell updates/sec

Title: US-09-001-737-8
Perfect score: 2663
Sequence: 1 MAKEIKFSADARAAMVRGVD.....TPAPAMPAGNDPMGMGMG 545

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2638	99.4	542	1	CH60_STRYP
2	2195.5	82.4	542	1	CH60_LACIA
3	2032.5	76.4	542	1	CH60_LISNO
4	2028.5	76.1	539	1	CH60_BAGST
5	2028.5	76.1	542	1	CH60_LISTN
6	2021.5	75.9	543	1	CH60_BACSD
7	2017.5	75.8	544	1	CH60_BACSD
8	1881	74.4	538	1	CH60_BACPD
9	1877.5	70.5	540	1	CH60_BACPD
10	1857.5	69.8	538	1	CH60_LACHE
11	1842.5	69.2	538	1	CH60_STAP
12	1833.5	68.9	540	1	CH60_CLOTH
13	1818	68.3	539	1	CH60_CLOTH
14	1776	66.7	543	1	CH60_CLOTH
15	1723.5	64.7	540	1	CH60_CLOTH
16	1697	64.1	542	1	CH60_CLOTH
17	1697	63.7	540	1	CH60_CLOTH
18	1688.5	63.4	545	1	CH60_CLOTH
19	1678.5	62.9	545	1	CH60_CLOTH
20	1672.5	62.9	545	1	CH60_CLOTH
21	1670.5	62.7	545	1	CH60_CLOTH
22	1670.5	62.7	546	1	CH60_CLOTH
23	1663.5	62.5	538	1	CH60_CLOTH
24	1661.5	62.4	544	1	CH60_CLOTH
25	1660	62.3	546	1	CH60_CLOTH
26	1657.5	62.2	545	1	CH60_CLOTH
27	1656	62.2	546	1	CH60_CLOTH
28	1656	62.2	547	1	CH60_CLOTH
29	1654	62.1	544	1	CH60_CLOTH
30	1653	62.0	547	1	CH60_CLOTH
31	1651	61.8	547	1	CH60_CLOTH
32	1646	61.8	539	1	CH60_CLOTH
33	1646	61.8	546	1	CH60_CLOTH

34	1646	61.8	546	1	CH60_BURTH	P58723 burkholderi
35	1643	61.7	547	1	CH60_BORPE	P48210 bordeletia
36	1642.5	61.7	539	1	CH62_MYCTU	P06806 mycobacteri
37	1642	61.7	546	1	CH60_BURCE	Q92760 burkholderi
38	1642	61.7	546	1	CH60_BURVI	Q92768 burkholderi
39	1641	61.6	546	1	CH60_NEIMB	P42385 neisseria m
40	1640.5	61.6	539	1	CH61_BRALJ	P77829 bradyrhizob
41	1640	61.6	547	1	CH60_ECOLI	P06139 escherichia
42	1639	61.5	543	1	CH62_SYNVU	Q57002 synechococc
43	1637	61.5	540	1	CH60_KLEPL	O66212 klebsiella
44	1636	61.4	544	1	CH60_NEIGO	P29842 neisseria g
45	1635.5	61.4	547	1	CH60_ALPHA	Q9xau7 alteromonas

ALIGNMENTS

RESULT 1
ID CH60_STRYP STANDARD; PRT; 542 AA.
AC P82485;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 60 kDa chaperonin (protein Cpn60) (GroEL protein).
GN GROL OR MOPR OR GROEL OR SPY2070.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP370 / ATCC 700294 / Serotype M1;
RX MEDLINE=1192684; PubMed=11296295;
RA Ferrerelli J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Olan Y., Jia H.G., Najjar F.Z., Ren O., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.M., Roe B.A., McLaughlin R., Song L., White J.,
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [2]
RP PARTIAL SEQUENCE AND MASS SPECTROMETRY.
RC STRAIN=DJSA / Serotype M6;
RA Hogan D.A., Du P., Stevenson T.I., Whilton M., Kilby G.W., Rogers J.,
RA Vanbogaert R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
proteins.";
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CONDITIONS (BY SIMILARITY).
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC EMBL: AE006627; AAK34727.1; -
CC HSSP: P06139; IGRL.
DR InterPro: IPR001844; Chaprin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP-1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTC1.
DR PROSITE: PS00296; CHAPERONIN_CPN60_1.
KW Chaperone: Heat shock: ATP-binding; Complete proteome.
FT INIT_MET 0

SO SEQUENCE 542 AA: 56964 MW: C7B9A13B6FD71DA CRC64:

Query Match 99.18; Score 2638; DB 1; Length 542;
 Best Local Similarity 99.88; Pred. No. 1,6e-114;
 Matches 540; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 AKEIKFSADARAAMRGVMDLADTVKVTLGPKGRNVVLEKAGSPFLTNDGVTIAKEIEI 61
 DB 1 AKDIKFSADARAAMRGVMDLADTVKVTLGPKGRNVVLEKAGSPFLTNDGVTIAKEIEI 60
 OY 62 EDHFNNGAKLVSEVASKTNDIAGDGTATATVLTQAIHVEGKANTGAPDGRGIEI 121
 DB 61 EDHFNNGAKLVSEVASKTNDIAGDGTATATVLTQAIHVEGKANTGAPDGRGIEI 120
 OY 122 ATATAVALKAIAPVSGKEATNOVAASVSRSEKVEYISEMERNGNDGVITIEESRG 181
 DB 121 ATATAVALKAIAPVSGKEATNOVAASVSRSEKVEYISEMERNGNDGVITIEESRG 180
 OY 182 ETELEVVEGMDPGYLSQYMTDNEKNVALEMPFLITDKKYSNIODILPLEEVLT 241
 DB 181 ETELEVVEGMDPGYLSQYMTDNEKNVALEMPFLITDKKYSNIODILPLEEVLT 240
 OY 242 NRPLLIADVDGEALPTLVNKIRGTNVAVAKAPGDRRKALMDIAIILTGTVITE 301
 DB 241 NRPLLIADVDGEALPTLVNKIRGTNVAVAKAPGDRRKALMDIAIILTGTVITE 300
 OY 302 DLGELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPRE 361
 DB 301 DLGELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPRE 360
 OY 362 KLOERLAKLAGVAIVKAPETALKEMKRIEDALNTRAAREEIVAGGTALITVI 421
 DB 361 KLOERLAKLAGVAIVKAPETALKEMKRIEDALNTRAAREEIVAGGTALITVI 420
 OY 422 EKVAALEEGDDATGRNIVRLAEPRVQIALNAGVSVYIDLKSPAGSGFNAATG 481
 DB 421 EKVAALEEGDDATGRNIVRLAEPRVQIALNAGVSVYIDLKSPAGSGFNAATG 480
 OY 482 WMDMITGTIIDPVYVTRSAIQNAASVSLITTEAVVANKPEPATPAPAMPMDPGMK 541
 DB 481 WMDMITGTIIDPVYVTRSAIQNAASVSLITTEAVVANKPEPATPAPAMPMDPGMK 540
 OY 542 G 542
 DB 541 G 541

RESULT 2
 ID CH60_LACIA STANDARD; PRT; 542 AA.
 AC P37282;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
 GN GROEL OR MOBA OR GROEL OR L0394.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9352268; PubMed=8486277;
 RA Klm S.G., Bate C.A.;
 RT "Cloning and sequencing of the Lactococcus lactis subsp. lactis
 RL groEL operon";
 RC Gene 127:121-126(1993).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=2135186; PubMed=11337471;
 RA Bolotin A., Wincker P., Manger S., Jallion O., Malarme K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus

RT Lactis sp. lactis IL1403.*;
 RL Genome Res. 11:731-753(2001).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -2- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC 7 SUBUNITS (BY SIMILARITY).
 CC -3- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 CC
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DR EMBL: X71132; CA50446.1;
 DR EMBL: AE006276; AA004492.1;
 DR PIR: S32106; S32106.
 DR PIR: J06661; J06661.
 DR HSSP: P06139; IGRL.
 DR InterPro: IPR001844; Chaperonin_Cpn60.
 DR InterPro: IPR002423; Cpn60_TCP1.
 DR Pfam: PF00118; Cpn60_TCP1.1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCOMPLEXTCP1.
 DR PROSITE: PS00296; CHAPERONIN_CPN60.1.
 KW Chaperone; ATP-binding; Complete proteome.
 FT CONFLICT 63 63 D -> V (IN REF. 1).
 FT CONFLICT 88 88 T -> N (IN REF. 1).
 FT CONFLICT 289 289 D -> H (IN REF. 1).
 FT CONFLICT 367 367 L -> V (IN REF. 1).
 FT CONFLICT 542 542 M -> I (IN REF. 1).
 SQ SEQUENCE 542 AA: 57201 MW: D7D6F5319DA59721 CRC64:

Query Match 82.48; Score 2195.5; DB 1; Length 542;
 Best Local Similarity 81.18; Pred. No. 3.2e-94;
 Matches 442; Conservative 52; Mismatches 46; Indels 5; Gaps 3;

OY 1 MAKEIKFSADARAAMRGVMDLADTVKVTLGPKGRNVVLEKAGSPFLTNDGVTIAKEIEI 60
 DB 1 MSKDIKFSADARAAMRGVMDLADTVKVTLGPKGRNVVLEKAGSPFLTNDGVTIAKEIEI 60
 OY 61 LEDHFNNGAKLVSEVASKTNDIAGDGTATATVLTQAIHVEGKANTGAPDGRGIEI 120
 DB 61 LEDHFNNGAKLVSEVASKTNDIAGDGTATATVLTQAIHVEGKANTGAPDGRGIEI 120
 OY 121 TATATAVALKAIAPVSGKEATNOVAASVSRSEKVEYISEMERNGNDGVITIEESRG 180
 DB 121 LAETAVASIKEMALPVHDKSAIQATVSSRSKVEYISDMERVSDDGVITIEESRG 180
 OY 181 MTELEVVEGMDPGYLSQYMTDNEKNVALEMPFLITDKKYSNIODILPLEEVLT 240
 DB 181 MTELEVVEGMDPGYLSQYMTDNEKNVALEMPFLITDKKYSNIODILPLEEVLT 240
 OY 241 TNRPLLIADVDGEALPTLVNKIRGTNVAVAKAPGDRRKALMDIAIILTGTVITE 300
 DB 241 TNRPLLIADVDGEALPTLVNKIRGTNVAVAKAPGDRRKALMDIAIILTGTVITE 300
 OY 301 EDGELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPRE 360
 DB 301 BELGLDKDATLEAAGAAKATVDKHTTIEGAGSADATSDRAVIAIKOIKETSDPRE 360
 OY 361 EKLDERLAKLAGVAIVKAPETALKEMKRIEDALNTRAAREEIVAGGTALITVI 420
 DB 361 EKLDERLAKLAGVAIVKAPETALKEMKRIEDALNTRAAREEIVAGGTALITVI 420
 OY 421 EKVAALEEGDDATGRNIVRLAEPRVQIALNAGVSVYIDLKSPAGSGFNAATG 480
 DB 421 INADKLSSEGIQIGINIVRLAEPRVQIALNAGVSVYIDLKSEEGVIGFNAATG 480
 OY 481 EMDMITGTIIDPVYVTRSAIQNAASVSLITTEAVVANKPEPATPAPAMPMDPGMK 540
 DB 481 EMDMITGTIIDPVYVTRSAIQNAASVSLITTEAVVANKPEPATPAPAMPMDPGMK 540

DB 481 CHVNMIEGIVDPKAVTYSALONNASVAGLITTEAVANKPEPA--APAPP-KDPSPH- 536
 QY 541 GGMG 545
 DB 537 -GGMG 540

RESULT 3
 CH60_LISMO STANDARD: PRT: 542 AA.
 ID CH60_LISMO
 AC 09AGE6;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
 GN GROEL OR GROEL OR LMO2068.
 OS Bacteria: Firmicutes; Bacillales; Listeriaceae; Listeria.
 NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LO28 / Serovar 1/2c;
 RX MEDLINE-21246697; PubMed-11349060;
 RA Gahan C.G., O'Mahony J., Hill C.;
 RT "Characterization of the groEL operon in Listeria monocytogenes:
 RT utilization of two reporter systems (gfp and hly) for evaluating in
 RT vivo expression.";
 RL Infect. Immun. 69:3924-3932(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EGD-e / Serovar 1/2a;
 RX MEDLINE-21537279; PubMed-11679669;
 RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Blocher H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Desautget O.,
 RA Entian K.-D., Faehl H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L.-M., Goebel W., Gomez-Lopez N., Hain T., Hain J., Jackson D.,
 RA Jones L., Kaerst U., Kreft J., Kuhn M., Kunst F., Kuriakka G.,
 RA Madueno E., Moutonnet A., Mota Vicente J., Ng E., Nedjari H.,
 RA Nordstedt G., Novella S., de Paulos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tietz A.,
 RA Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC 7 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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 DR EMBL: AF333323; AK28538.1;
 DR EMBL: AF591982; CAD00146.1;
 DR HSSP: P06139.1;GRL;
 DR Listlist: LMO02068;
 DR Interpro: IPR001844; Chaperonin.Cpn60.
 DR Interpro: IPR002423; Cpn60/TCPI-1.
 DR Pfam: PF00118; Cpn60/TCPI-1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCOMPLEXTCP1.
 DR PROSITE: PS00296; CHAPERONIN5_CPN60.1.
 KW Chaperone; ATP-binding; Complete proteome.
 SO SEQUENCE 542 AA; 57367 MW; 981845967D92944 CRC64;

Query Match 76.4%; Score 2033.5; DB 1; Length 542;
 Best Local Similarity 75.6%; Pred. No. 8.5e-87;
 Matches 412; Conservative 61; Mismatches 67; Indels 5; Gaps 3;

QY 1 MAKEIFSDARAAWAGVMDLADVVYLTGPGKRWVLEKAFGSPPLINDGVITAKEIE 60
 DB 1 MAKDIFSESDARRAMRGVDLANAVKTLGPGRNRYLEKKGSPPLINDGVITAKEIE 60
 QY 61 LEDPFENNGAKVSEVASKINDIAGDGTATATVLAQVHBDGKNTAGANIGIRGIE 120
 DB 61 LEDPFENNGAKVSEVASKINDVAGDGTATATVLAQMIQGLKNTAGANPVGRGIE 120
 QY 121 TATATPVALKATAPYVSKREIAQVAAVSSREKYEISEAMERNVNDGVITIEESRG 180
 DB 121 KAVATRIELKATSKPIESKESIAQVAAISSGDEEGLIAEMERNVNDGVITIEESRG 180
 QY 181 METELEVEGAGQEDRGYISQYVWTDNKKVYADLNPFLITDKKVSINDILPLEEVK 240
 DB 181 FATELDVVEGQDFDRGYTSYVWTDSDKMEAVLEKPYLITDKKINNIOELIPVLEQVQ 240
 QY 241 TNRPLLIADVDGALPTLVLNKTRGTFNVVAVAPGCDRRKAMLEDIALLTGVTIT 300
 DB 241 QGRPHLIADVEDEGAQATLVNKRGTFFNVVAVAPGCDRRKAMLEDIALLTGQVIT 300
 QY 301 EDGLLELDATWPTALGAAKITVDKSTVVEGSSSAIANRILIKSLQLETTSPDFOR 360
 DB 301 EDGLLELDATVDPGLTANKVYVTKDDTIVSAGDSYQISANVQINRAQMEITSEFR 360
 QY 361 EKLOERLAKLAGVAVIKYGAPTEALKEMKLRIDALNTPRAVEGIVAGGTALITY 420
 DB 361 EKLOERLAKLAGVAVYKAGATETELKEKLRIDALNTPRAVEGIVAGGTALITY 420
 QY 421 IEVVALELEDGATGRNIVLRALEEPYQIALNNGYGSVIDKDKSPAGTGFNAATG 480
 DB 421 YKNVVALELEDGATGRNIVLRALEEPYQIALNNGYGSVIDKDKSPAGTGFNAATG 480
 QY 481 EYVDIKTKTIDPVKYSALONNASVAGLITTEAVANKPEPATPAPAMPDGRM 540
 DB 481 EYVNMIDGIVDPKAVTYSALONNASVAGLITTEAVANKPEPATPAPAMPDGRM 540
 QY 541 GGMG 545
 DB 536 GGMG 540

RESULT 4
 CH60_BACST STANDARD: PRT: 539 AA.
 ID CH60_BACST
 AC 007201;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
 GN GROEL OR GROEL OR GROEL.
 OS Bacillus stearothermophilus.
 NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-N0836;
 RX MEDLINE-93224474; PubMed-8096841;
 RA Schoen U., Schumann W.;
 RT "Molecular cloning, sequencing, and transcriptional analysis of the
 RT groEL operon from Bacillus stearothermophilus.";
 RL J. Bacteriol. 175:2465-2469(1993).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC 7 SUBUNITS (BY SIMILARITY).
 CC -1- INDUCTION: BY HEAT SHOCK.
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

[illegible]

QY 361 EKLOERLAKIAGVAVIVKAPETALKEMLRIEDALNTRAIVEGIVAGGATLITV 420
 Db 361 EKLOERLAKIAGVAVIVKAPETALKEMLRIEDALNTRAIVEGIVAGGATLITV 420
 QY 421 IEKVALEEGDDAGRCRIVYALKEEPVQALNAGRESSVYIDKLKSPAGCFNAATG 480
 Db 421 YNKVALEEGDVEGTINIVKRSLEEPVQALNAGRESSVYIERLKEHAYGVGFNAANG 480
 QY 481 EMDMKTGIIIDPVKVTYSALQNAVASLITTEAVVANKPEPAPAPAMPAGMDPGM 540
 Db 481 EMDMKTGIIIDPVKVTYSALQNAVASLITTEAVVANKPEPAPAPAMPAGMDPGM 540
 QY 541 GGMGG 545
 Db 536 GGMGG 540
 RESULT 6
 CH60_BACSU STANDARD: PRT: 543 AA.
 ID CH60_BACSU
 AC P28598: 005526;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (protein Cpn60) (groEL protein) (Stress protein H5).
 GN GROEL OR MOXA OR GROEL.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OX NCBI_TaxID:1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92283754; PubMed-1350777;
 RA Schmidt A., Schlesswohl M., Voelker U., Hecker M., Schumann W.;
 RT "Cloning, sequencing, mapping, and transcriptional analysis of the
 RT groEL operon from Bacillus subtilis.";
 RL J. Bacteriol. 174:3993-3999(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE-92283753; PubMed-1350776;
 RA Li M., Wong S.L.;
 RT "Cloning and characterization of the groEL operon from Bacillus
 RT subtilis.";
 RL J. Bacteriol. 174:3981-3992(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE-9312952; PubMed-1369494;
 RA Tozawa Y., Yoshikawa H., Kawamura F., Itaya M., Takahashi H.;
 RT "Isolation and characterization of the groES and groEL genes of
 RT Bacillus subtilis Marburg.";
 RL Biosci. Biotechnol. Biochem. 56:1995-2002(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / Marburg;
 RX MEDLINE-98116660; PubMed-9455482;
 RA Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadale Y.;
 RT "Sequence analysis of the groEL-coca region of the Bacillus subtilis
 RT genome, containing the restriction/modification system genes.";
 RL DNA Res. 4:335-339(1997).
 RN [5]
 RP SEQUENCE OF 1-18 FROM N.A.
 RC STRAIN-168 / Marburg;
 RX MEDLINE-97345038; PubMed-9202461;
 RA Sadale Y., Yata K., Fujita K., Segal H., Itaya M., Kasahara Y.,
 RA Ogasawara N.;
 RT "Nucleotide sequence and analysis of the phoB-trmE-groEL region of
 RT the Bacillus subtilis chromosome.";
 RL Microbiology 143:1861-1866(1997).
 RN [6]
 RP SEQUENCE OF 1-30.
 RC STRAIN-168 / IS58;
 RX MEDLINE-94282319; PubMed-8012595;

RA Voelker U., Engelmann S., Maul B., Rietdorf S., Voelker A.,
 RA Schmidt R., Mach H., Hecker M.;
 RT "Analysis of the induction of general stress proteins of Bacillus
 RT subtilis.";
 RL Microbiology 140:741-752(1994).
 RN [7]
 RP SEQUENCE OF 1-30.
 RC STRAIN-168 / IS58;
 RX MEDLINE-93123969; PubMed-1362210;
 RA Voelker U., Mach H., Schmidt R., Hecker M.;
 RT "Stress proteins and cross-protection by heat shock and salt stress
 RT in Bacillus subtilis.";
 RL J. Gen. Microbiol. 138:2125-2135(1992).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC 7 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

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 or send an email to license@isb.slb.ch).
 CC EMBL: M84965; AAA22531.1;
 DR EMBL: M81332; AAA22503.1;
 DR EMBL: D10972; BAA22519.1;
 DR EMBL: AB007637; BAA22747.1;
 DR EMBL: D88802; BAA19727.1;
 DR EMBL: Z99107; CAB12422.1;
 DR PIR: B41884; B41884;
 DR PIR: B41885; B41885;
 DR PIR: JCI372; JCI372;
 DR HSSP: P06139; IGRL.
 DR Subtilist: BGI0423; groL.
 DR InterPro: IPR001844; Chaperonin.Cpn60.
 DR InterPro: IPR002423; Cpn60/TCF-1.
 DR Pfam: PF00118; cpn60_TCF1.1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCOMPLEXTCF1.
 DR PROSITE: PS00296; CHAPERONIN60.CPN60; 1.
 KW Chaperone; ATP-binding; Heat shock; Complete proteome.
 FT INIT_MER 0
 FT CONFLICT 14 14 M -> N (IN REF. 3).
 FT CONFLICT 124 124 V -> L (IN REF. 3).
 FT CONFLICT 201 201 M -> L (IN REF. 3).
 FT CONFLICT 374 374 A -> R (IN REF. 3).
 SQ SEQUENCE 543 AA; 57293 MW; 587259578FF3800 CRC64.

Query Match 75.9%; Score 2021.5; DB 1; Length 543;
 Best Local Similarity 73.7%; Pred No. 3e-66;

Matches 401; Conservative 69; Mismatches 71; Indels 3; Gaps 1;
 QY 2 AKRIFSDAAMVAGVAMLDVYKTLDPGRNVYLERAFSPILINDGYITAKIEI 61
 Db 1 AKRIFSEARALRGVADLADVAKVTLDPGRNVYLERAFSPILINDGYITAKIEI 60
 QY 62 EDHFENMGAKLIVSEVASKTNDIADGTTATVYLAIVHESGLKNVATGANDPIGRIGET 121
 Db 61 EDHFENMGAKLIVSEVASKTNDIADGTTATVYLAIVHESGLKNVATGANDPIGRIGET 120
 QY 122 AATAVEALKAIQPVYSGKEALIAQVAVSSRSKVEYISPMAREGNDGYITTEESRCM 181
 Db 121 AATAVEALKAIQPVYSGKEALIAQVAVSSRSKVEYISPMAREGNDGYITTEESRCM 180
 QY 182 ETELEVVGKQDFRGYLSQYVWTNENKRVADLENFYLITDKVSNIDYIPLLEEVLT 241
 Db 181 ETELEVVGKQDFRGYLSQYVWTNENKRVADLENFYLITDKVSNIDYIPLLEEVLT 240

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OY 242 NRPLLIADVDGALPTLVNKIRGTNNVAVAKAFGDRRKAMLEDAITLGGTYTE 301
DB 241 GKPLLIADVEGALATLVNKLGTNNVAVAKAFGDRRKAMLEDAITLVGEVITE 300
OY 302 DLGLELKDATMTALGOAKITVDKSTIYVSGSSSEAIANRILIKSOLETTSSDRE 361
DB 301 DLGLDLSKSTQIOLQGRASKVYVTKENTTYEGAGETDKISARVQIAQVETTSSEDR 360
OY 362 KLEERLAKLAGVAVIKVGAPEETALKEKRIEDLNATRAVEEGYVAGGCTALTIV 421
DB 361 KLEERLAKLAGVAVIKVGAPEETALKEKRIEDLNATRAVEEGYVAGGCTALTIV 420
OY 422 EKVALELEGGDAGRIVYRALPEPVOIALAGVEGVYIDKLNKSPAGTGNATGE 481
DB 421 NKRAAVEAGSAGOTGINIVYRALPEPVOIALAGVEGVYIDKLNKSPAGTGNATGE 480
OY 482 VWMHITGTIDPVKVTYRSALONASVASLITTEAVVANKPEPATPAPMGDPGGM 541
DB 481 VWMHITGTIDPVKVTYRSALONASVASLITTEAVVANKPEPATPAPMGDPGGM 537
OY 542 GMMG 545
DB 538 GMMG 541

RESULT 7
CH60_BACHD STANDARD: PRT: 544 AA.
ID 050305; 09KFC3;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN GROEL OR MOPR OR GROEL OR BH0562.
OS Bacillus halodurans
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=97141316; PubMed=8987660.
RA Xu L., Kobayashi T., Kudo T.;
RT Molecular cloning and nucleotide sequence of the groEL gene from the
RL alkaliphilic Bacillus sp. strain C-125 and reactivation of thermally
RL inactivated alpha-glucosidase by recombinant groEL."
RL Biosci. Biotechnol. Biochem. 60:1633-1636(1996).
RN 2;
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC
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DB EMBL, D55630, BAA09494.1;

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DR EMBL: AP001508; BAA04281.1;
DR HSSP: P06139; 1GRF.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.
DR PRINTS: PR00296; CHAPERONIN60.
DR PRINTS: PR00304; TCP1EXTRC1.
DR PROSITE: PS00296; CHAPERONIN_CPN60_1.
KM Chaperone: ATP-binding; Heat shock; Complete proteome.
FT CONFLICT 407 407 E -> VK (IN REF. 1).
FT CONFLICT 421 421 MISSING (IN REF. 1).
FT FT 500 500 A -> VP (IN REF. 1).
FT CONFLICT 512 512 MISSING (IN REF. 1).
SQ SEQUENCE 544 AA: 57403 MW; C769ED81C903C971 CRC64;

Query Match 75.8%; Score 2017.5; DB 1; Length 544;
Best Local Similarity 73.4%; Pred. No. 4,6e-86;
Matches 400; Conservative 74; Mismatches 68; Indels 3; Gaps 1;

OY 1 MAKEIRFSADARAARVRCVMDLADYKVTIGPKGRNVLEKAFSGSPILTDGTYIKKE 60
DB 1 MAKDKFSEDAARSMRLRGVDKLDADVKYTLGPKGRNVLEKAFSGSPILTDGTYIKKE 60
OY 61 LEDHEFMGAKLYSEVASKNDIAGDGTATVLTQAIYHEGLKAVTAGANPIGIRGIE 120
DB 61 LEDAFEMGAKLYSEVASKNDIAGDGTATVLTQAIYHEGLKAVTAGANPIGIRGIE 120
OY 121 TATATAVEALKAIADPVSGKEAIAOVAAYSSRSSEKVEYISBAMERVGNDGVITIEESRG 180
DB 121 KATVAAVEELSKISPIEGKDSIAOVAAYSSRSSEKVEYISBAMERVGNDGVITIEESRG 180
OY 181 METELEVEVGMPDGRGLSOYVWTVNDEKRVADLENPIITLDKRVSNIDILPLEEYVK 240
DB 181 FSTLEVEVGMPDGRGLSOYVWTVNDEKRVADLENPIITLDKRVSNIDILPLEEYVK 240
OY 241 TNRPLLIADVDGALPTLVNKIRGTNNVAVAKAFGDRRKAMLEDAITLGGTYIT 300
DB 241 OGRPILIIADVEGALATLVNKLGTNNVAVAKAFGDRRKAMLEDAITLVGEVITE 300
OY 301 EDLGLLELKDATMTALGOAKITVDKSTIYVSGSSSEAIANRILIKSOLETTSSDRE 360
DB 301 EDLGLLELKDATMTALGOAKITVDKSTIYVSGSSSEAIANRILIKSOLETTSSDRE 360
OY 361 EKLDERLAKLAGVAVIKVGAPEETALKEKRIEDLNATRAVEEGYVAGGCTALTIV 420
DB 361 EKLDERLAKLAGVAVIKVGAPEETALKEKRIEDLNATRAVEEGYVAGGCTALTIV 420
OY 421 EKVALELEGGDAGRIVYRALPEPVOIALAGVEGVYIDKLNKSPAGTGNATGE 480
DB 421 IKAVSSIGAGDEGATGINIVYRALPEPVOIALAGVEGVYIDKLNKSPAGTGNATGE 480
OY 481 EYWDKRTGTIDPVKVTYRSALONASVASLITTEAVVANKPEPATPAPMGDPGGM 540
DB 481 EYWDKRTGTIDPVKVTYRSALONASVASLITTEAVVANKPEPATPAPMGDPGGM 537
OY 541 GMMG 545
DB 538 GMMG 542

RESULT 8
CH60_BACP3 STANDARD: PRT: 538 AA.
ID 01-MAY-1992 (Rel. 22, Created)
AC P26209;
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock 61 kDa
DE protein).
GN GROEL OR MOPR OR GROEL.
OS Bacillus PS3 (Thermophilic bacterium PS-3).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=70306;

```

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91354309; PubMed-1679330;
 RA Tamada H., Ohta T., Hamamoto T., Otawara Hamamoto Y., Yanagi M.,
 RA Hirata H., Hirata H., Kaseya Y.,
 RT *Gene structure of heat shock proteins 61kDa and 12kDa (thermophilic
 RT chaperonins) of the thermophilic bacterium P33.
 RT Biochem Biophys Res Commun. 19:365-371(1991).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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 CC
 DR EMBL: S57424; AAB2915.2; ALT_SEQ.
 DR PIR: J01195; J01195.
 DR HSRP: P06139; IGRU.
 DR Interpro: IPR001844; Chaperln_Cpn60.
 DR Interpro: IPR002423; Cpn60/TCF-1.
 DR Pfam: PF00118; Cpn60_TCF1; 1.
 DR PRINTS: PRO0298; CHAPERONIN60.
 DR PRINTS: PRO0304; TCOMPLEXTCF1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
 KW Chaperone; ATP-binding; Heat shock.
 SQ SEQUENCE 538 AA; 57182 MW; 516C97ACBA227103 CRC64;

Query Match 74.4%; Score 1981; DB 1; Length 538;
 Best Local Similarity 73.7%; Pred. No. 2,2e+8;

Matches 400; Conservative 64; Mismatches 73; Indels 6; Gaps 1;

Oy 1 MAKEIKFSADARAAVGVYDMLADYVYTLGPRGRNVYLEKAFSPITINDGYTAKTE 60
 Db 1 MAKQIFSEBARMLRGVYDLADYVYTLGPRGRNVYLEKAFSPITINDGYTAKTE 60
 Oy 61 LEDHFNMGAKLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNVYAGNPVIGIRGIE 120
 Db 61 LEDHFNMGAKLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNVYAGNPVIGIRGIE 120
 Oy 121 TATATAVEALKAIAQPVSGKEAIAQVAVSSRSSEKVEYISEAMERYGNDGYTIEESRG 180
 Db 121 KAVAAVAVELKAISKPKRESIAQVAIAISADAEVGLIEMAMERYGNDGYTIEESRG 180
 Oy 181 METELEVEVGMQDFRGYLSQYVWTDNKKVADLENFLLITDKVSNIDILPLEEVLK 240
 Db 181 FTELEDEVEGMQDFRGYSPVNMITDEKMAVLENNYILITDKVSIQELLPALQVYQ 240
 Oy 241 TNRPLLIADVDGEALPTLVNKRIGTFNVVYKAPGGRKRAMLEIDAILTGTVIT 300
 Db 241 OGRPLLIADVEGEALATLVNKRIGTFNVVYKAPGGRKRAMLEIDAILTGTVIS 300
 Oy 301 EDGLGLMDATMTALGOAKITVYDSDYVIEGSGSEAIKRNALIKSOLTTTSPDFR 360
 Db 301 EELGRELKSTIASLGSRASKVYTTKETTTIVBAGDSKRIKAIINQIRKLETTSEDFR 360
 Oy 361 EKIOERLAKLAGVYATYKGAETELAKEMKLEIDALNATRAAVEBGVAGGTALITV 420
 Db 361 EKIOERLAKLAGVYATYKGAETELAKEMKLEIDALNATRAAVEBGVAGGTALITV 420
 Oy 421 IENVALELEDGDDATGRTNIVLRALEEPYROIALNAGYSGSVYIDKLKNSPAGTFNATG 480
 Db 421 HNKVAIAIEAGDEATGYKIVLRAIEEPYROIALNAGYSGSVYIDKLKNSPAGTFNATG 480
 Oy 481 EWDNMIKTGIIDPVKYVRSALONASVASTLITTEVAANPEEPATPAMPAGMDGGM 540
 Db 481 EWDNMIKTGIIDPVKYVRSALONASVASTLITTEVAANPEEPATPAMPAGMDGGM 540

Db 481 EWDNMIKTGIIDPVKYVRSALONASVASTLITTEVAANPEEPATPAMPAGMDGGM-----M 534
 Oy 541 GGM 543
 Db 535 GGM 537
 RESULT 9
 CH60_LACHE
 ID CH60_LACHE STANDARD; PRT; 540 AA.
 AC 068324;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
 GN GROEL OR MOXA OR GROEL.
 OS Lactobacillus helveticus.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 CX NCBI_TaxID=1587;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LH212;
 RX MEDLINE-98439363; PubMed-9766226;
 RA Broadbent J.R., Oberg C.J., Wel L.;
 RT *Characterization of the Lactobacillus helveticus groEL operon.*;
 RL Res. Microbiol. 149:247-253(1998).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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 CC
 DR EMBL: AF031929; AAC29004.1; .
 DR HSRP: P06139; IGRU.
 DR Interpro: IPR001844; Chaperln_Cpn60.
 DR Interpro: IPR002423; Cpn60/TCF-1.
 DR Pfam: PF00118; Cpn60_TCF1; 1.
 DR PRINTS: PRO0298; CHAPERONIN60.
 DR PRINTS: PRO0304; TCOMPLEXTCF1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
 KW Chaperone; ATP-binding.
 SQ SEQUENCE 540 AA; 57638 MW; 42570DB45FC7C4B4 CRC64;

Query Match 70.5%; Score 1877.5; DB 1; Length 540;
 Best Local Similarity 70.5%; Pred. No. 1,2e+79;

Matches 382; Conservative 68; Mismatches 87; Indels 5; Gaps 3;

Oy 1 MAKEIKFSADARAAVGVYDMLADYVYTLGPRGRNVYLEKAFSPITINDGYTAKTE 60
 Db 1 MAKQIFSEBARMLRGVYDLADYVYTLGPRGRNVYLEKAFSPITINDGYTAKTE 60
 Oy 61 LEDHFNMGAKLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNVYAGNPVIGIRGIE 120
 Db 61 LEDHFNMGAKLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNVYAGNPVIGIRGIE 120
 Oy 121 TATATAVEALKAIAQPVSGKEAIAQVAVSSRSSEKVEYISEAMERYGNDGYTIEESRG 180
 Db 121 KAVAAVAVELKAISKPKRESIAQVAIAISADAEVGLIEMAMERYGNDGYTIEESRG 180
 Oy 181 METELEVEVGMQDFRGYLSQYVWTDNKKVADLENFLLITDKVSNIDILPLEEVLK 240
 Db 181 FTELEDEVEGMQDFRGYSPVNMITDEKMAVLENNYILITDKVSIQELLPALQVYQ 240

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OY 241 TNRPLLIADVDGALPTLVNKRGTGNTVAVAKAGFGDRKRMEDIALITGGTIT 300
DB 241 OGRSLLIADDTIGELALPTLVNKRGTGNTVAVAKAGFGDRKRMEDIALITGGTIT 300
OY 301 EDGLLEKDATATGALGAAKITVDKSTIVYEGSSSEAIANNALISQLETTIDFPR 360
DB 301 EDGLLEKDATATGALGAAKITVDKSTIVYEGSSSEAIANNALISQLETTIDFPR 360
OY 361 EKLOERLAKLAGAVAVKAPETALKEMLKRIEDLNTRAIVEGIVAGGTAITV 420
DB 361 EKLOERLAKLAGAVAVKAPETALKEMLKRIEDLNTRAIVEGIVAGGTAITV 420
OY 421 IEKVAALEEG---DQATGRNIVRALPEPVOIALAGESVVIDKLKNSAGTGFA 477
DB 421 -BK-AVEVAGETTDGOTGINIVYRALSPVOIALAGESVVIDKLKNSAGTGFA 478
OY 478 AGGEVIMITGIDPVKVTASALONASVASLITTEAVVANKPEPATPAMPAGMDP 537
DB 478 AKDKENKAVDAGIDPTVYTRTALONASIASIALLTTEAVVAEIEPPOAAGGAGAM 538
OY 538 GM 539
DB 539 GM 540

RESULT 10
CH60_STRAEP STANDARD: PRT: 538 AA.
AC P48218:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein 60).
GN GROEL OR MOXA OR GROEL OR HSP60.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9759.
RA COH S.H., Wood J., Hemmingsen S., Chow A.W.;
RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC -----
DR EMBL: U13618; AAA2134.1; -
DR HSP60; P06139; IGRU.
DR InterPro: IPR001844; Chapernin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1_1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTC1.
DR PROSITE: PS00296; CHAPERONINS_CPN60_1.
KW Chaperone; ATP-binding; Heat shock.
FT INITMET 0 BY SIMILARITY.
SQ SEQUENCE 538 AA; 57518 MW; 8DAAE9A62446C8E6 CRC64;
Query Match 69.8%; Score 1857.5; DB 1; Length 538;
Best Local Similarity 67.3%; Pred. No. 1e-78;

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Matches 363; Conservative 87; Mismatches 88; Indels 1; Gaps 1.
OY 2 AKIKRFSADAAAVGVMLADPVYKTLGPKRRNVLEKAFSGPLITIDGTTAKIEL 61
DB 1 AKIKRFSADAAVGVMLADPVYKTLGPKRRNVLEKAFSGPLITIDGTTAKIEL 60
OY 62 EDHFENKAKVSYVASKNDIADGTTATVYTOAIYHEGLKNVTAGANPIGRIGET 121
DB 61 EDHFENKAKVSYVASKNDIADGTTATVYTOAIYHEGLKNVTAGANPIGRIGET 120
OY 122 ATFAVEALKAIAOPVSGKEALAOVAVSSRSEKVEYISSEAMERVNDGVTIEESRG 181
DB 121 AVOVALEALHISCKVENKNEALAOVAISADEIGRISSEAMDKVNGVITIEESNGF 180
OY 182 ETELEVGMOPFCYLSQVMTDNEKRVADLENPFILITDKKVNIODILPLEEVLKT 241
DB 181 NTELEVAGMOPFCYLSQVMTDNEKRVADLENPFILITDKKVNIODILPLEEVLKT 240
OY 242 NREPLIADVDGALPTLVNKRGTGNTVAVAKAGFGDRKRMEDIALITGGTIT 301
DB 241 NREPLIADVDGALPTLVNKRGTGNTVAVAKAGFGDRKRMEDIALITGGTIT 300
OY 302 DLGLEKDATATGALGAAKITVDKSTIVYEGSSSEAIANNALISQLETTIDFPR 361
DB 301 DLGLEKDATATGALGAAKITVDKSTIVYEGSSSEAIANNALISQLETTIDFPR 360
OY 362 EKLOERLAKLAGAVAVKAPETALKEMLKRIEDLNTRAIVEGIVAGGTAITV 421
DB 361 EKLOERLAKLAGAVAVKAPETALKEMLKRIEDLNTRAIVEGIVAGGTAITV 420
OY 421 IEKVAALEEGDQATGRNIVRALPEPVOIALAGESVVIDKLKNSAGTGFA 481
DB 421 IEKVAALEEGDQATGRNIVRALPEPVOIALAGESVVIDKLKNSAGTGFA 480
OY 481 WDMIKTGIIDPVKVTASALONASVASLITTEAVVANKPEPATPAMPAGMDP 540
DB 481 WDMIKTGIIDPVKVTASALONASVASLITTEAVVANKPEPATPAMPAGMDP 538

RESULT 11
CH60_STRAU STANDARD: PRT: 538 AA.
AC Q08854;
DT 01-FEB-1994 (Rel. 30, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein 60).
GN GROEL OR MOXA OR GROEL OR HSP60.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=912;
RX MEDLINE=93290669; Pubmed=7916607;
RA Ohta T., Honda K., Kuroda M., Saito K., Hayashi H.;
RL Molecular characterization of the gene operon of heat shock proteins
RT HSP60 and HSP10 in methicillin-resistant Staphylococcus aureus.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REPRODING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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DR EMBL: D14711; BAA03533.1;
 DR PIR: JN0601; JN0601.
 DR HSP: P06139; 1GRU.
 DR InterPro: IPR001844; Chaperonin_Cpn60.
 DR InterPro: IPR002423; Cpn60/TCP-1.
 DR Pfam: PF00118; Cpn60_TCP1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCOMPLEXTCP1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
 DR Chaperone: ATP-binding; Heat shock.
 FT INIT_MET 0
 FT SEQUENCE 538 AA; 5722 MW; 58173E21A6EALCSE CRC64;

Query Match 69.2%; Score 1842.5; DB 1; Length 538;
 Best Local Similarity 68.4%; Pred. No. 4.9e-78;
 Matches 370; Conservative 78; Mismatches 86; Indels 7; Gaps 4;

OY 3 KEIKTSADARAARAGVDMLADTVKVLGKGNVYLEKAGSPILITNDGVTIAKEIELE 62
 DB 2 KQKTSFEDRQMLRGVDOLANAVYIGRGNNVLDKFTAPLITNDGVTIAKEIELE 61
 OY 63 DHEENNGAKLYSEVASKTNDIAGDGTATATVLTQAIHVEGLKNVYAGANPIGRIGIETA 122
 DB 62 DPEENNGAKLYSEVASKTNDIAGDGTATATVLTQAIHVEGLKNVYAGANPIGRIGIETA 121
 OY 123 TATAVEALKAIAPVSGKEAIAOYAAVSSRSKEVGEYISEAMERVNDGV--ITIEESR 179
 DB 122 VKYAVEALHENSOKVENKNEINQVGAISADEEIGYISEATEVENDGVITITIEESN 181
 OY 180 GMELEVEVGMQFDGYSLOYWYTDNEKNVADLENPILITTDKKSNIODITPLEEVY 239
 DB 182 RLNTLEEL--GMQFDGYSLOYWYTDNEKNVADLENPILITTDKKSNIODITPLEEVY 239
 OY 240 KTRPRLIITADVDGALPTLVKIRGTFTNVYAVKAPGCDPRKMLDIAITLGSTVY 299
 DB 240 QSNRPILIVADVEGDLNITVLRMGSTFTVAVKAPGCDPRKMLDIAITLGSTVY 299
 OY 300 TEDLGLKDTMTALGOAKITVDKSTYIYEGSGSEAIANRILITLSOLETTSDDE 359
 DB 300 TDGLGLKDTMTALGOAKITVDKSTYIYEGSGSEAIANRILITLSOLETTSDDE 359
 OY 360 REKLOERLAKIAGVAVIVGAPETALKEMLRIEDALNATRAVEEGIVAGGTALIT 419
 DB 360 REKLOERLAKIAGVAVIVGAPETALKEMLRIEDALNATRAVEEGIVAGGTALIT 419
 OY 420 VIEKVALELEGGDATGRNIVLRALPEPVROIALNAGYEGSVYIDILKSPAGTGAAT 479
 DB 420 VYOKVSENEAEGDIETGVAVILKALZAPVQOIAENAGLEGSIVERTLKAEPGVNGAT 479
 OY 480 GEMVMDIKTGIIDPVKVTSAIQNAASVASLITIEAVVANKREPTAPAPAMPMPGDC 539
 DB 480 NEMVMDIKTGIIDPVKVTSAIQNAASVASLITIEAVVANKREPTAPAPAMPMPGDC 539
 OY 540 M 540
 DB 538 M 538

RESULT 12

CH60_CLOTM STANDARD; PRT; 540 AA.
 AC P48212;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (HSP-60).
 GN GROL OR MOPA OR GROL.
 OS Clostridium thermocellum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium
 OX NCBI_TaxID=1515;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-NCIB 10682;
 RA MEDLINE=97199381; PubMed=9047357;
 RA Citrele A., Cross S., Freedman R.B., Hazlewood G.P.;
 RT Sequence and transcriptional analysis of groES and groEL genes from
 RL the thermophilic bacterium Clostridium thermocellum.
 RL Gene 186:143-147(1997).
 RP SEQUENCE OF 1-20
 RC STRAIN-NCIB 10682;
 RA MEDLINE=9625758; PubMed=8687408;
 RA Cross S.J., Citrele A., Pomputsa K., Romaniec M.P.M., Freedman R.B.;
 RL Thermostable chaperonin from Clostridium thermocellum.
 RL Biochem. J. 316:615-622(1996).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC 7 SUBUNITS.
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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 CC or send an email to license@lsb-sdb.ch.)
 DR EMBL: Z68137; CA9242.1;
 DR HSP: P06139; 1GRU.
 DR InterPro: IPR001844; Chaperonin_Cpn60.
 DR InterPro: IPR002423; Cpn60/TCP-1.
 DR Pfam: PF00118; Cpn60_TCP1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCOMPLEXTCP1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
 DR Chaperone: ATP-binding.
 FT INIT_MET 0
 FT CONFLICT 14 15 LE -> ML (IN REF. 2).
 FT CONFLICT 20 20 Q -> K (IN REF. 2).
 FT SEQUENCE 540 AA; 57343 MW; A638C71A2675C596 CRC64;
 Query Match 68.9%; Score 1833.5; DB 1; Length 540;
 Best Local Similarity 68.4%; Pred. No. 1.3e-77;
 Matches 372; Conservative 77; Mismatches 88; Indels 7; Gaps 2;

OY 2 AKETKSADARAARAGVDMLADTVKVLGKGNVYLEKAGSPILITNDGVTIAKEIELE 61
 DB 1 AKQKTSFEDRQMLRGVDOLANAVYIGRGNNVLDKFTAPLITNDGVTIAKEIELE 60
 OY 62 DHEENNGAKLYSEVASKTNDIAGDGTATATVLTQAIHVEGLKNVYAGANPIGRIGIETA 121
 DB 61 DPEENNGAKLYSEVASKTNDIAGDGTATATVLTQAIHVEGLKNVYAGANPIGRIGIETA 120
 OY 122 TATAVEALKAIAPVSGKEAIAOYAAVSSRSKEVGEYISEAMERVNDGVITIEESRGM 181
 DB 121 AVDAVAEGIKELISQVKNVGEDIAFVASISANDEIETLADAMEKVTNDGVITIEEATM 180
 OY 182 ETELEVEVGMQFDGYSLOYWYTDNEKNVADLENPILITTDKKSNIODITPLEEVYKT 241
 DB 181 CTNLEIVEGMQFDGYSLOYWYTDNEKNVADLENPILITTDKKSNIODITPLEEVYQO 240
 OY 242 NRPLIITADVDGALPTLVKIRGTFTNVYAVKAPGCDPRKMLDIAITLGSTVY 301
 DB 241 GKRLIITADVDGALPTLVKIRGTFTNVYAVKAPGCDPRKMLDIAITLGSTVY 300
 OY 302 DLGELKDTMTALGOAKITVDKSTYIYEGSGSEAIANRILITLSOLETTSDDE 361
 DB 301 DLGELKDTMTALGOAKITVDKSTYIYEGSGSEAIANRILITLSOLETTSDDE 360

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Oy 362 KLEERLAKGAVAVIKVAPETETALKEMKRIEDALNTRAIVEGIVAGGATLITVY 421
Db 361 KLEERLAKGAVAVIOVGAATEETEMKRIEDALNTRAIVEGIVAGGATLITVY 420
Oy 422 EKVAAAL--ELEGGDATTGRNIVLRALPEEPROJALNAGYEGSVYIKLNSPAGTGNMAT 479
Db 421 PVAIVADTVYSGDEKTVGVIILRLALEEPVROJALNAGLBSGVYIKVYASPEIGDADVN 480
Oy 480 GEMVDMIKTGIIDPYKTRRSALNAAVSALITTEAVANKPEEPATAPAMPAGNDPM 539
Db 481 EKVYVMLEAGTIDPKVTRRSALNAAVSALITTEAVADPEKETSIGPGAG----- 535
Oy 540 MCGM 543
Db 536 MCGM 539

RESULT 13
CH60.CLOPE STANDARD: PRT: 539 AA.
ID CH60.CLOPE STANDARD: PRT: 539 AA.
AC P26821.
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN GROEL OR MOXA OR GROEL OR CPE2289.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
CX Clostridium.
RN NCBI_Taxid:1502;
RP SEQUENCE FROM N.A.
RX MEDLINE-92182020; PubMed-1347462;
RA Ruenigawa E., Singh B., Gupta R.S.;
RT "Cloning of Hsp60 (groEL) operon from Clostridium perfringens using a
RL polymerase chain reaction based approach.";
RL Biochim. Biophys. Acta 1130:90-94(1992).
RN 121
RP SEQUENCE FROM N.A.
RX STRAIN-13 / Type A;
RA PubMed-11792842;
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Yamashita H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC -----
DR EMBL: X62914; CAA44697.1;
DR EMBL: AP003193; BAB81995.1;
DR PIR: S18869; S18869.
DR PIR: S22342; S22342.
DR HSSP: P06139; 1GRU.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR Pfam: PF00118; Cpn60_TCP1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONIN60_CPN60.1.

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KW Chaperone: ATP-binding; Complete proteome.
FT CONFLICT 344 V->I (IN REF. 1).
SQ SEQUENCE 539 AA: 57366 MR: E649BC7DD1DEE29 CRC64:
Query Match 68.3%, Score 1618; DB 1; Length 539;
Best Local Similarity 67.3%, Pred. No. 6,56-77;
Matches 366; Conservative 78; Mismatches 92; Indels 6; Gaps 2;
Oy 1 MAKEIKFSADRAARAVRGVMDLADTVKVLGPRGRNVVLEKAFSGPLITNDGVITAKEIE 60
Db 1 MATTLFEEERSRSMQGVKDLANTVAVTLGPRGRNVVLDKFKFSPLITNDGVITAREIE 60
Oy 61 LEDHEENKGAALYSEVASKTNDIAGDGTATATVLTQALVIEGKLNATAGANPIGIRGIE 120
Db 61 LEDAVENNGAQLVEKAVATKINDVAGDGTATATLTAQALIRREGKLVNTAGANPILIRNGIK 120
Oy 121 TATATAVALKAAIQPVSGKEATIQVAAVSRSREKVEYISEAMERVNDGVITIEESRG 180
Db 121 TAVEKAVEIEOKISKPVNGKEDIRVAALISADEKICGLTADMEKVEYITVEESKS 180
Oy 181 METELEVEGEGMOPDRGYLSQYMTNDKRYADLENPILLTDKVSNIQDILPLEEVK 240
Db 181 METELDVYEGMOPDRGYLSAIVYDTEKMEAVLDNPVLITDKKISNIQDILPLEEVQ 240
Oy 241 TTRPLLITADYVGEALPLVLYKINGTNNVAVKAPGCDRRKAMLEDIALITGTIVT 300
Db 241 ACKRLILITADIDIGEMMTLVNKLKGTFCVGAAPGFDRRKEMLDITLTVGVVIS 300
Oy 301 EDGLLEKDKATMALGOAAKITVDKDSIVIEGSGSEBAIANTRIALINSOLETTSDPR 360
Db 301 DEVGDDLEKATITLDMIGEAESVYKSTTIVNGRNSSEIKNRVNDIKLEATTSDFDK 360
Oy 361 EKLDERLAKGAVAVIKVAPETETALKEMKRIEDALNTRAIVEGIVAGGATLITVY 420
Db 361 EKLDERLAKGAVAVIVGAAETETELKESKRIEDALNTRAIVEGIVAGGATVAVVY 420
Oy 421 IEKVAALELE-GDDATGRNIVLRALPEEPROJALNAGYEGSVYIKLNSPAGTGNMAT 479
Db 421 INEVAKLSDIQDEQGINIIVSLEEPVROJALNAGLBSGVYIEKVNDSAGIGDALR 480
Oy 480 GEMVDMIKTGIIDPYKTRRSALNAAVSALITTEAVANKPEEPATAPAMPAGNDPM 539
Db 481 GEMVDMIKATIDPKVTRRSALNAAVSALITTEAVADPE-----KEMPGAGMGM 535
Oy 540 MCGM 541
Db 536 MCGM 537

RESULT 14
CH60.CLOAB STANDARD: PRT: 543 AA.
ID CH60.CLOAB STANDARD: PRT: 543 AA.
AC P30717.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN GROEL OR MOXA OR GROEL OR CAC2703.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
CX Clostridium.
RN NCBI_Taxid:1488;
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 4259 / DSM 1731 / NCIB 619;
RX MEDLINE-92250424; PubMed-1349602;
RA Netherhaus F., Bahl H.;
RT "Cloning, sequencing, and molecular analysis of the groEL operon of
RL Clostridium acetobutylicum.";
RN 121
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

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RX MEDLINE-21359325; PubMed-11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hittl J., Wolf Y.I.,
RA Talusov R.L., Sabath F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.
RL J. Bacteriol. 183:4823-4838(2001).
CC
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC
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CC
DR EMBL: M74572; AAA23243.1;
DR EMBL: AE007768; AKK80649.1;
DR PIR: B41872; B41872.
DR HSP: P06139; 1GRL.
DR InterPro: IPR001844; Chaperlin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONIN60.
DR Chaperone; ATP-binding; Complete proteome.
KM
SEQUENCE 543 AA; 58073 MW; 6FD16C2EBD0A03DAC CRC64;
SQ
Query Match 66.7%; Score 1776; DB 1; Length 543;
Best Local Similarity 66.3%; Pred. No. 5.5e-75;
Matches 362; Conservative 78; Mismatches 100; Indels 6; Gaps 4;
QY 1 MAKEIFSADARAAMVGVNMLADTVKVLGPKGNVYLGKAGSPILITNGVYTIKREI 60
DB 1 MAKOLYGEARSRMOKGVNLDVTKVTLGPKGNVYLDKKGAPLITNGVSIKKEI 60
QY 61 LEDHFENMGAKLYSEVASKTNDIAGDGTATVLTQAIYHEGILKAVTAGAPICIRGIE 120
DB 61 LEDPEKMGAGLYKVEAKTKTDVAGDGTITATLQAIYHEGILKAVTAGAPILIRNGIR 120
QY 121 TATATAVEALKAIAOPVSGKATIAOVAANSSSEKVEYISEMERVNDGVITIEESRG 180
DB 121 TAVDKTYEGLKAKVSKNKGKEDARVASISADPEIKLADMEKRVNEGVITIEESKS 180
QY 181 METELEVEVGKQFDRGYLSQYWTDNKKVADLENPELITTKKVSNIOTDITPLEEVK 240
DB 181 MGTLEDVVEGKQFDRGYLSPTWYTDKKMEANLDDPYLITTKKIANIOETDITPLEQIYV 240
QY 241 TNRPLLIIADVGEALPTVLTAKIRGTFNVVAVAKAGFDRKRLMEDIALITGGTVT 300
DB 241 OGKRLIADVGEALATLVYKRLGTFNCVAVAKAGFDRKRLMEDIALITGGEVIS 300
QY 301 EDLGLLELDKATWTALGQAKITVDKSTVIEGSGSEALANRILALISOLEFTTSDFPR 360
DB 301 EELGLDKLVKVEDLGSASEVSKIKSENTIYNGSGDSAIHBRVAINGOEETTSDFPR 360
QY 361 EKLOERLAKLAGGAVAVIKVAGPTEFTLTKEMKRLIEDLNAATRAAEETIYVAGGTLITV 420
DB 361 EKLOERLAKLAGGAVAVIKVAGPTEFTLTKEMKRLIEDLNAATRAAEETIYVAGGTLITV 420
QY 421 IEKVAALEL-EGDDATGNNIYLALEEPYROIALINAGYEGSVIDKLKNSPAGTGNAT 479
DB 421 LPEVRELTSDEPVOVGINTIVALEEPYROIALINAGLESVIEIKIINSEKIGFDALH 480
QY 480 GEVWDMITGIIIDPVKVTISALONAAVASLITLTTAEVAVANKPEAPAPAMPAGMDPGM 539

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DB 481 EKIVDMISGIVDIPKVTISALONAAVASLITLTTCAVADIPE--KDKPEMGGA-EGM 537
QY 540 MGGMG 545
DB 538 --GGMG 541
DB 538 --GGMG 541
RESULT 15
CH60_THEBR STANDARD; PRT; 540 AA.
ID CH60_THEBR
AC 060024;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (protein Cpn60) (groEL protein).
GN GROEL OR MOBA OR GROEL
OS Thermanaerobacter brockii (Thermanaerobium brockii).
OC Bacteria; Firmicutes; Clostridia; Thermanaerobacteriales;
OC Thermanaerobacteriaceae; Thermanaerobacter.
OX NCBI_TaxID=29323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RT8_G4.
RX MEDLINE-99014232; PubMed-9795109;
RA Truscott K.N., Scopes R.K.;
RT "Sequence analysis and heterologous expression of the groE genes from
RT Thermanaerobacter sp. RT8_G4."
RL Gene 217:15-23(1998).
RN [2]
RP SEQUENCE OF 1-43, AND CHARACTERIZATION.
RC STRAIN=RT8_G4.
RX MEDLINE-94291621; PubMed-7912671;
RA Truscott K.N., Hoeg P.B., Scopes R.K.;
RT "Purification and characterization of chaperonin 60 and chaperonin 10
RT from the anaerobic thermophile Thermanaerobacter brockii."
RL Eur. J. Biochem. 222:277-284(1994).
RN [3]
RP -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
RP PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
RP CONDITIONS (BY SIMILARITY).
RP
RP -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
RP 7 SUBUNITS (BY SIMILARITY).
RP
RP -1- MASS SPECTROMETRY: MW=57949; MW-ERR=10; METHOD=Electrospray.
RP
RP -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
RP
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CC
DR EMBL: U56021; BAB00559.1;
DR HSP: P06139; 1GRL.
DR InterPro: IPR001844; Chaperlin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONIN60.
DR Chaperone; ATP-binding; Complete proteome.
KM
INIT_MET 0
FT INIT_MET 0
FT SEQUENCE 540 AA; 57928 MW; 27C316MD5C61734 CRC64;
SQ
Query Match 64.7%; Score 1723.5; DB 1; Length 540;
Best Local Similarity 64.9%; Pred. No. 1.4e-72;
Matches 349; Conservative 80; Mismatches 106; Indels 3; Gaps 2;
QY 2 AKKIFESADARAAMVGVNMLADTVKVLGPKGNVYLGKAGSPILITNDGVTAKRIEL 61
DB 1 AKOLYGEARSRMOKGVNLDVTKVTLGPKGNVYLDKKGAPLITNDGVTAKRIEL 60

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OY 62 EDHEENKALYSEVASTNDIAGDCTTATVLTQAIWHEGLKNTAGANPIRGITET 121
DB 61 EDPENOGAQLKEATNTNDIAGDGTATLTLQAAMVREGKLNLAGANPMLLRGIAR 120
OY 122 ATATVETALKAIAPVSGKEAIAOVAASNSKEVGEYISEAMERVNDGVITIEESRGM 181
DB 121 AVDAVETGLKRISKIDNKRESIAHVASISADEEIGKILAEAMDYKGDGVITIEESKTL 180
OY 182 ETELEVVEGMOFDRGYLSOYVVTDNKEMVADLENPFILITDKKVSNIQDILPLEEVLT 241
DB 181 GTLEVEGMOFDRGYISPYVVTDAKEMBAVLEEPVILITDKKISNIQDILPLEEIOVQ 240
OY 242 NRPLIADVDGEALPTLVNKRIGCTENVVAVAKPGFDRKRALEDIAILITGGVYTE 301
DB 241 GKLLIADVDGEALPTLVNKRIGCTENVVAVAKPGFDRKRALEDIAILITGGVYTE 300
OY 302 DLGELKDATMTALGOAKITVDKOSTYVEGSSSEAIANRIALIKSOLETTSDPRE 361
DB 301 ELGYDLKDVRLDMGRAROVKYTEYITVGGADPSEIKRKNQIKAOIEETSDYDRE 360
OY 362 KLOERLAKLAGVAVIKVAPETALKEKRLIEDALNTRAVEGIVAGGTALITVI 421
DB 361 KLOERLAKLAGVAVIOGAETTELKKEKRIEDALNTRAVEGIVAGGTALITVI 420
OY 422 EKVAL--ELEGDATGNTIVLPALEEPVROIALNAGYEGSVIDKLKS-PAGTFNAA 478
DB 421 EDVOKVVDLEDEFTAKIVLPALEEPVROIATNAGVDGSYIYERIKAKDPNFGYDAY 480
OY 479 TGEVDMIRKTIIDPVVTRISALONNASVSLITTEAVVANKPEPATPAPAMPAGMD 536
DB 481 KEETDMFRAGIVDPFTVTRIALONNASIASMILTTEAIVDIDPEKNTGMPNPGAGMD 538

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Job time : 16 secs